



Genetic and epigenetic alterations induced by different levels of rye genome integration in wheat recipient

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ABSTRACT. The narrow genetic variation present in common wheat (*Triticum aestivum*) varieties has greatly restricted the improvement of crop yield in modern breeding systems. Alien addition lines have proven to be an effective means to broaden the genetic diversity of common wheat. Wheat-rye addition lines, which are the direct bridge materials for wheat improvement, have been widely used to produce new wheat cultivars carrying alien rye germplasm. In this study, we investigated the genetic and epigenetic alterations in two sets of wheat-rye disomic addition lines (1R-7R) and the corresponding triticales. We used expressed sequence tag-simple sequence repeat, amplified fragment length polymorphism, and methylation-sensitive amplification polymorphism analyses to analyze the effects of the introduction of alien chromosomes (either the entire genome or sub-genome) to wheat genetic background. We found obvious and diversiform variations in the genomic primary structure, as well as alterations in the extent and

pattern of the genomic DNA methylation of the recipient. Meanwhile, these results also showed that introduction of different rye chromosomes could induce different genetic and epigenetic alterations in its recipient, and the genetic background of the parents is an important factor for genomic and epigenetic variation induced by alien chromosome addition.

Key words: Wheat-rye addition lines; Genetic alterations; Epigenetic alterations